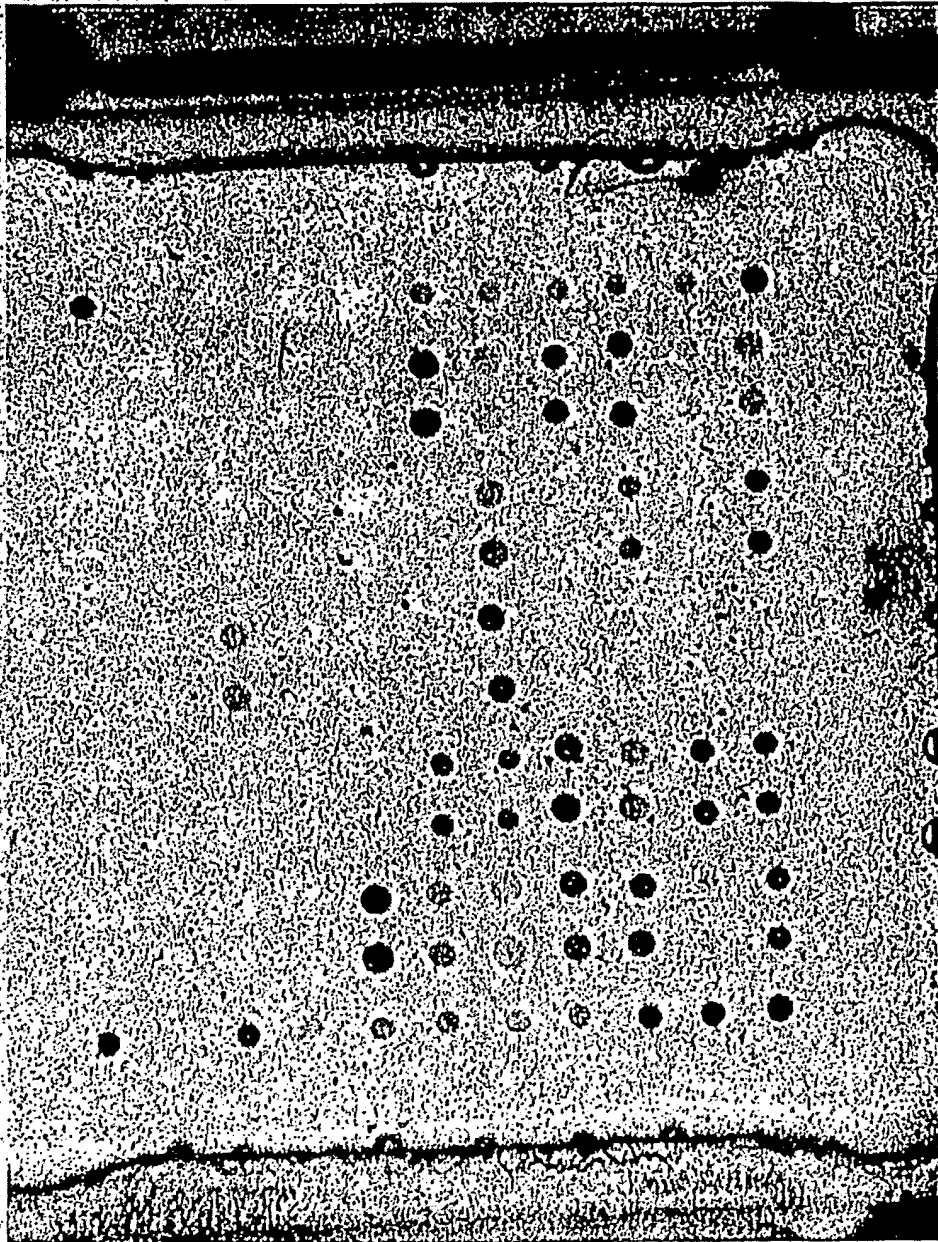


Fig.1

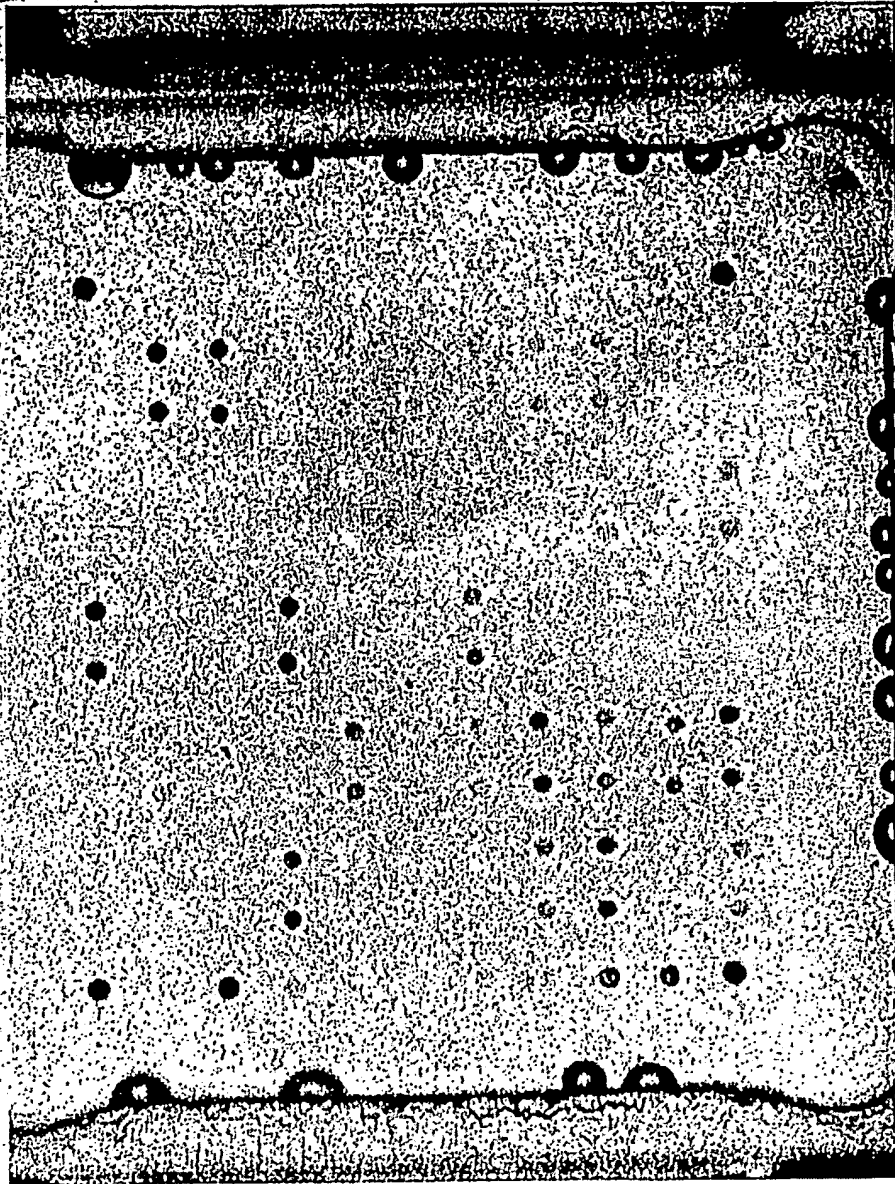
P. aeruginosa AT-Chip



ZW117

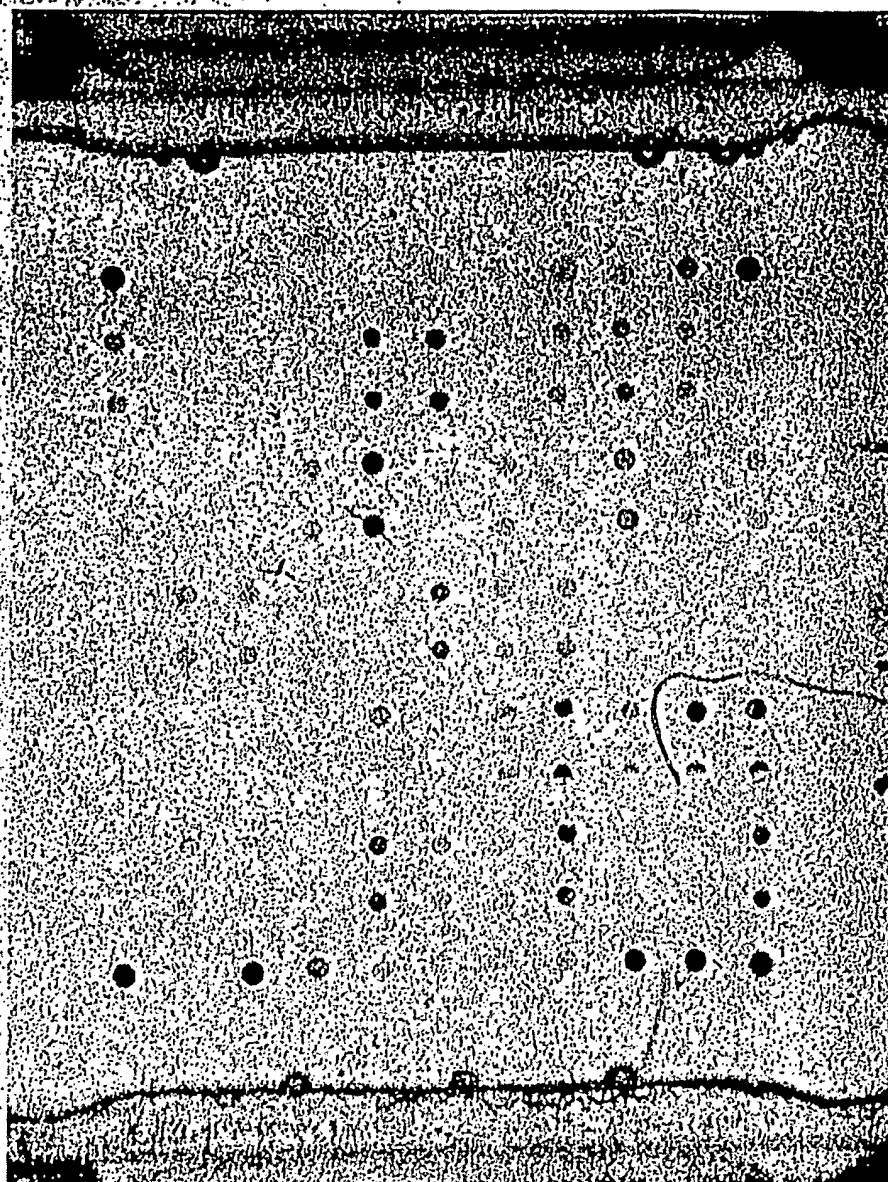
Fig.2

P. aeruginosa AT-Chip



RP17

P. aeruginosa AT-Chip



TB

P. aeruginosa AT-Chip

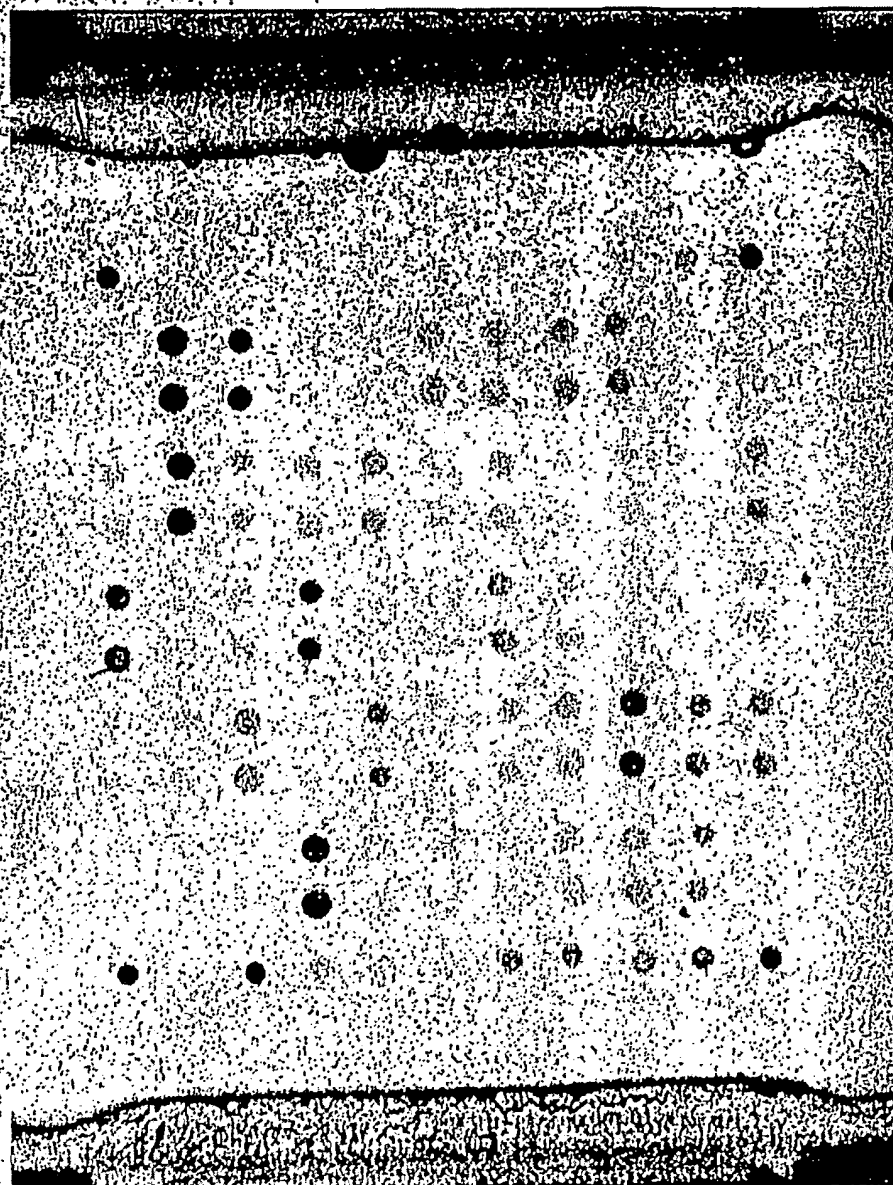


Fig.4

SG17M

P. aeruginosa AT-Chip

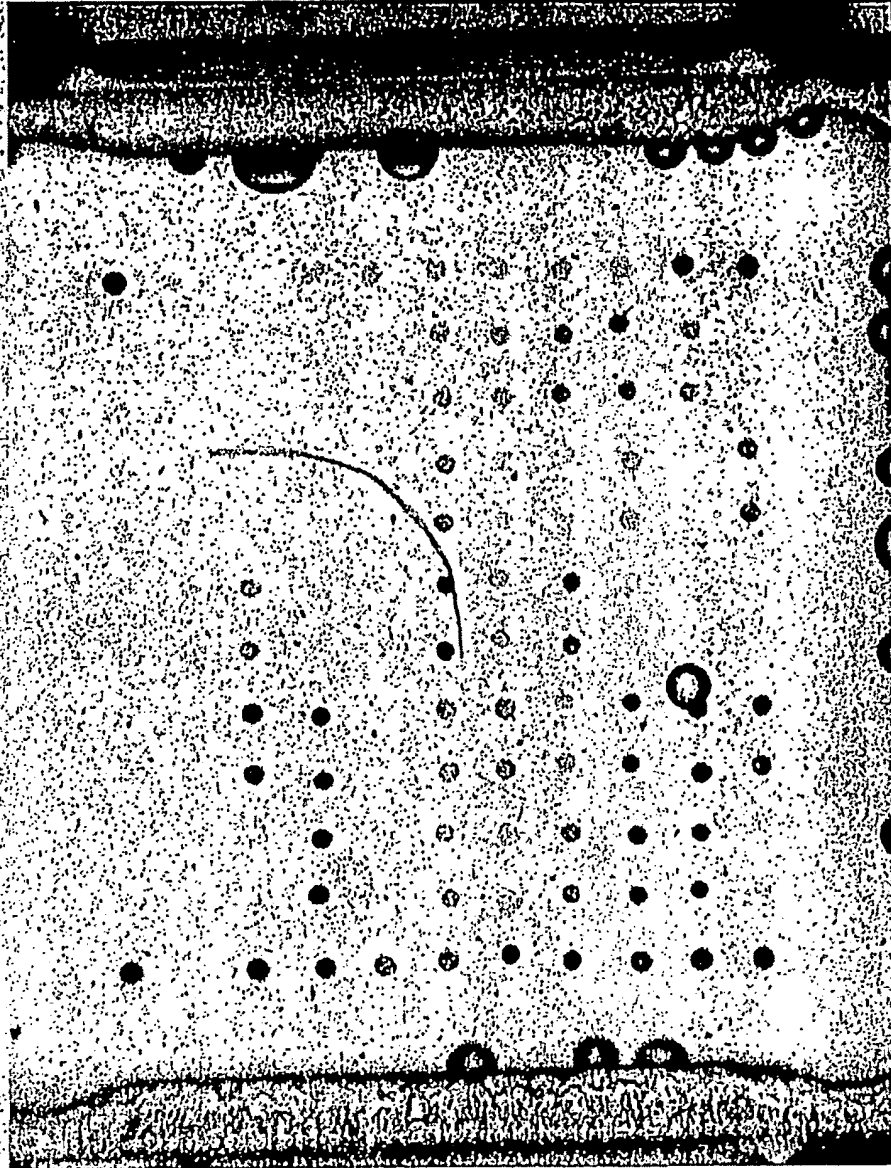
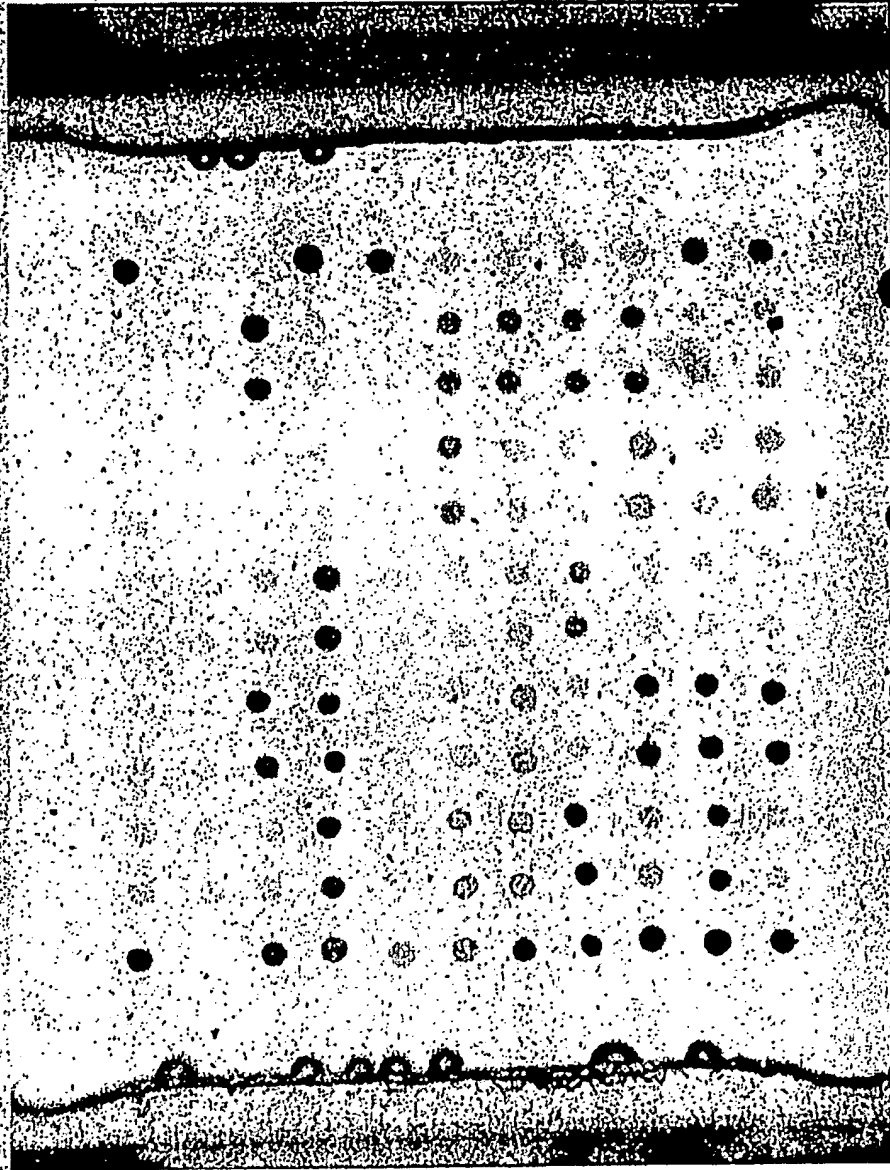


Fig.5

BST85

Fig.6

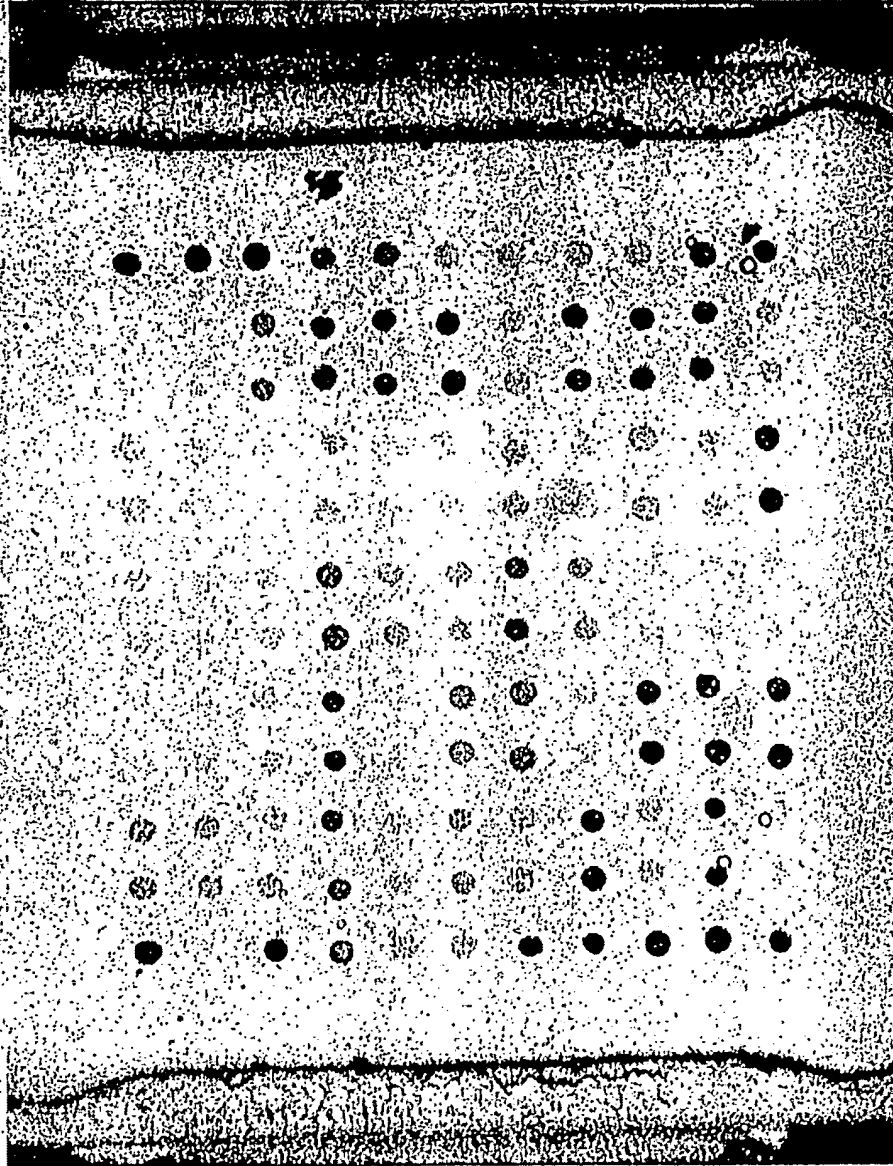
P. aeruginosa AT-Chip



AL5846

Fig.7

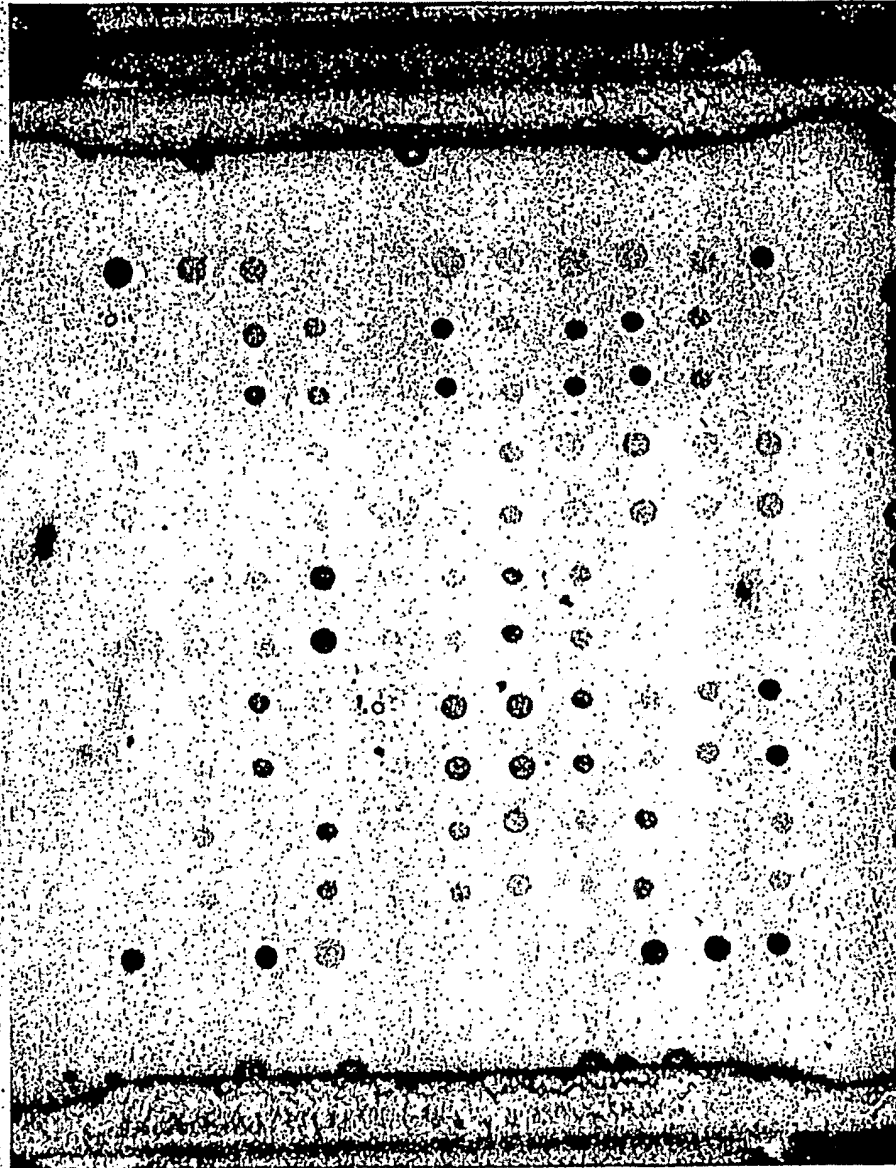
P. aeruginosa AT-Chip



PT12

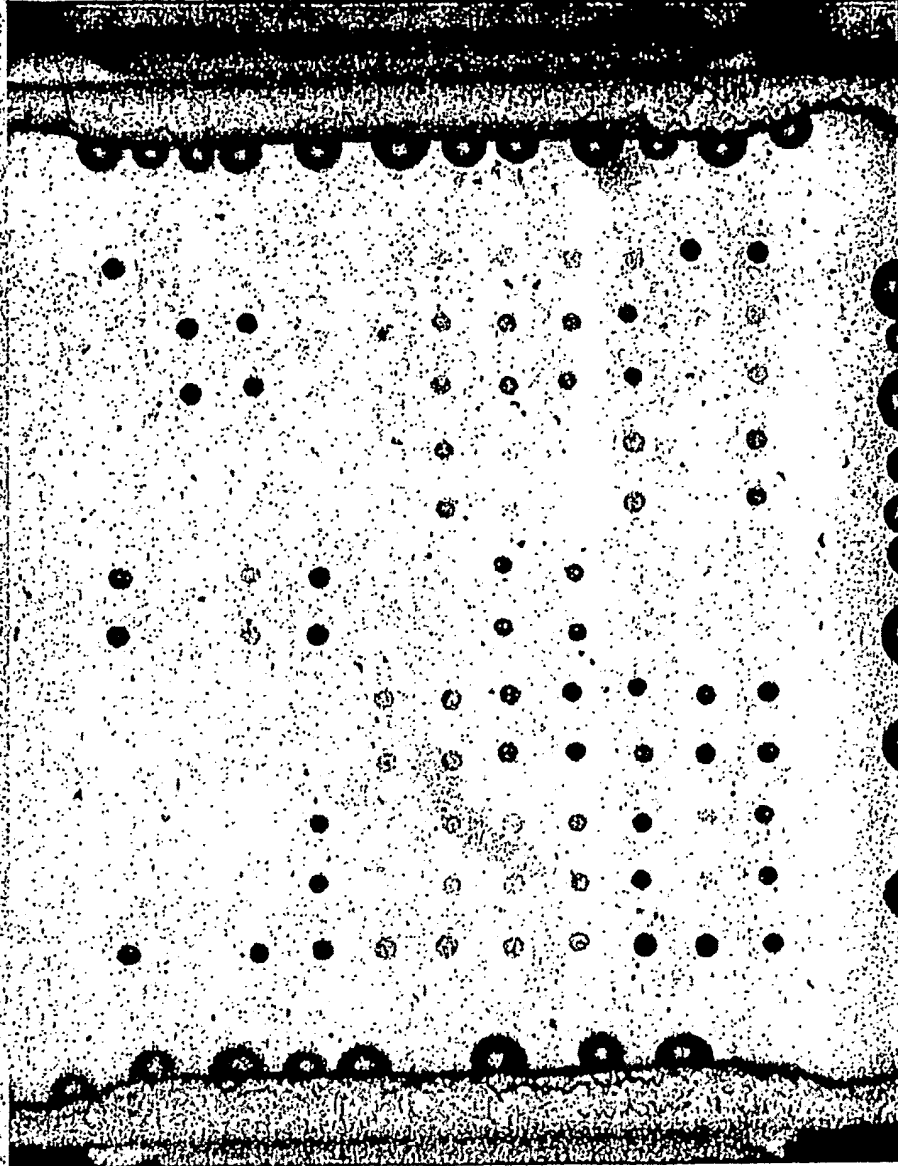
Fig.8

P. aeruginosa AT-Chip



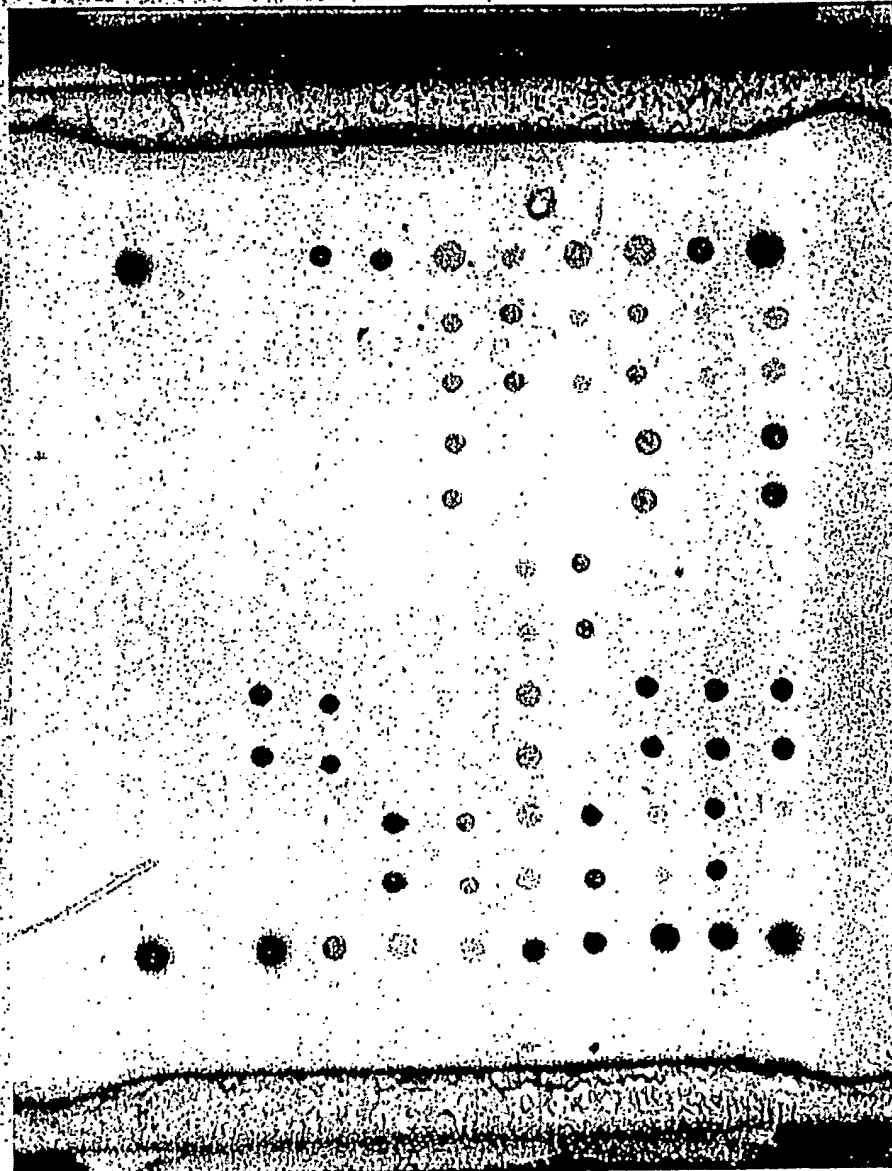
PT20

P. aeruginosa AT-Chip



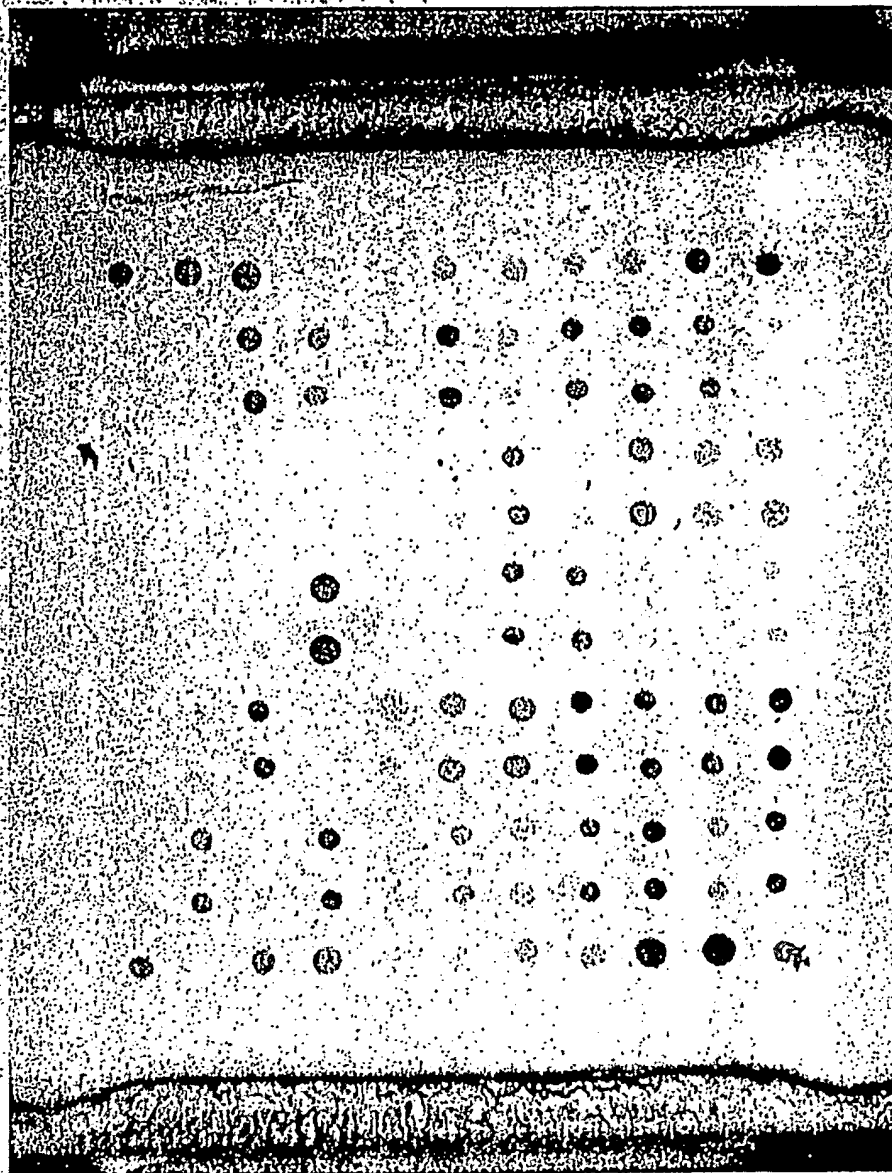
ZW79

P. aeruginosa AT-Chip



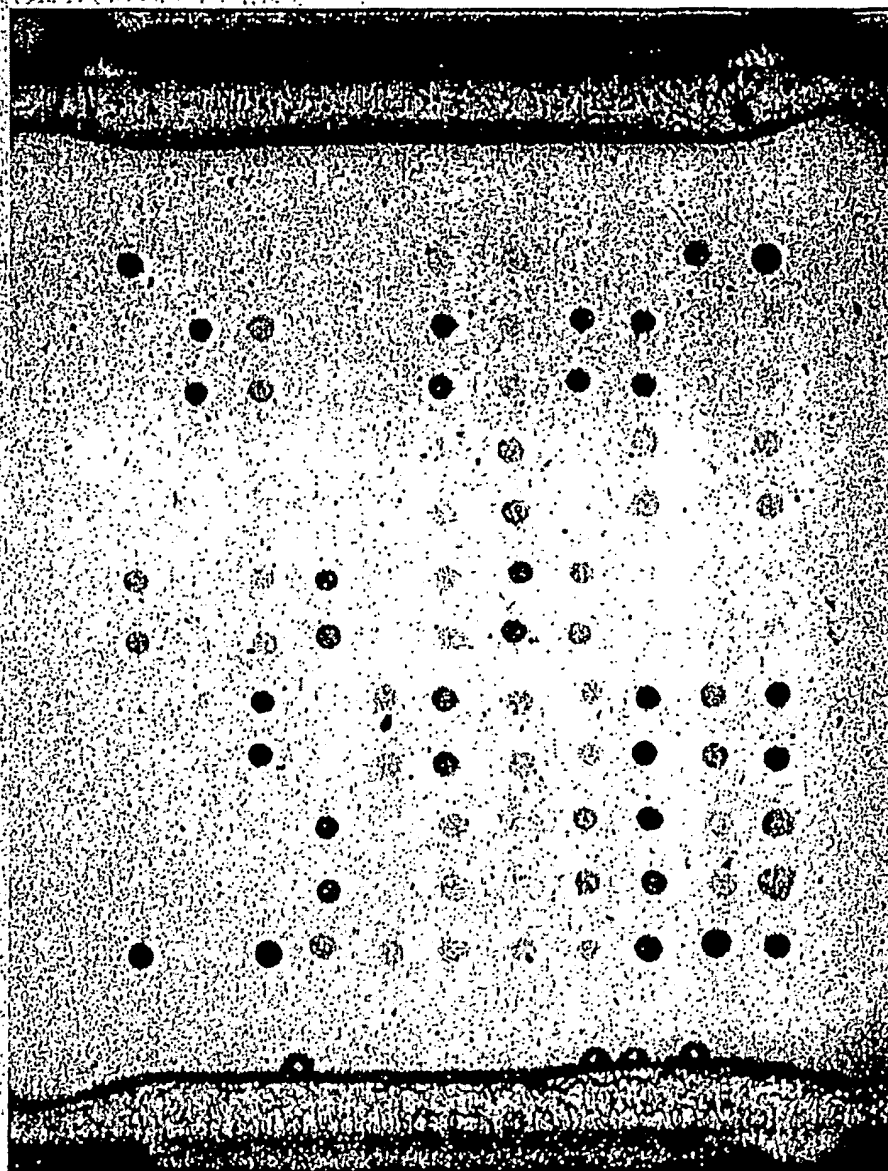
ZW85

P. aeruginosa AT-Chip



2813A

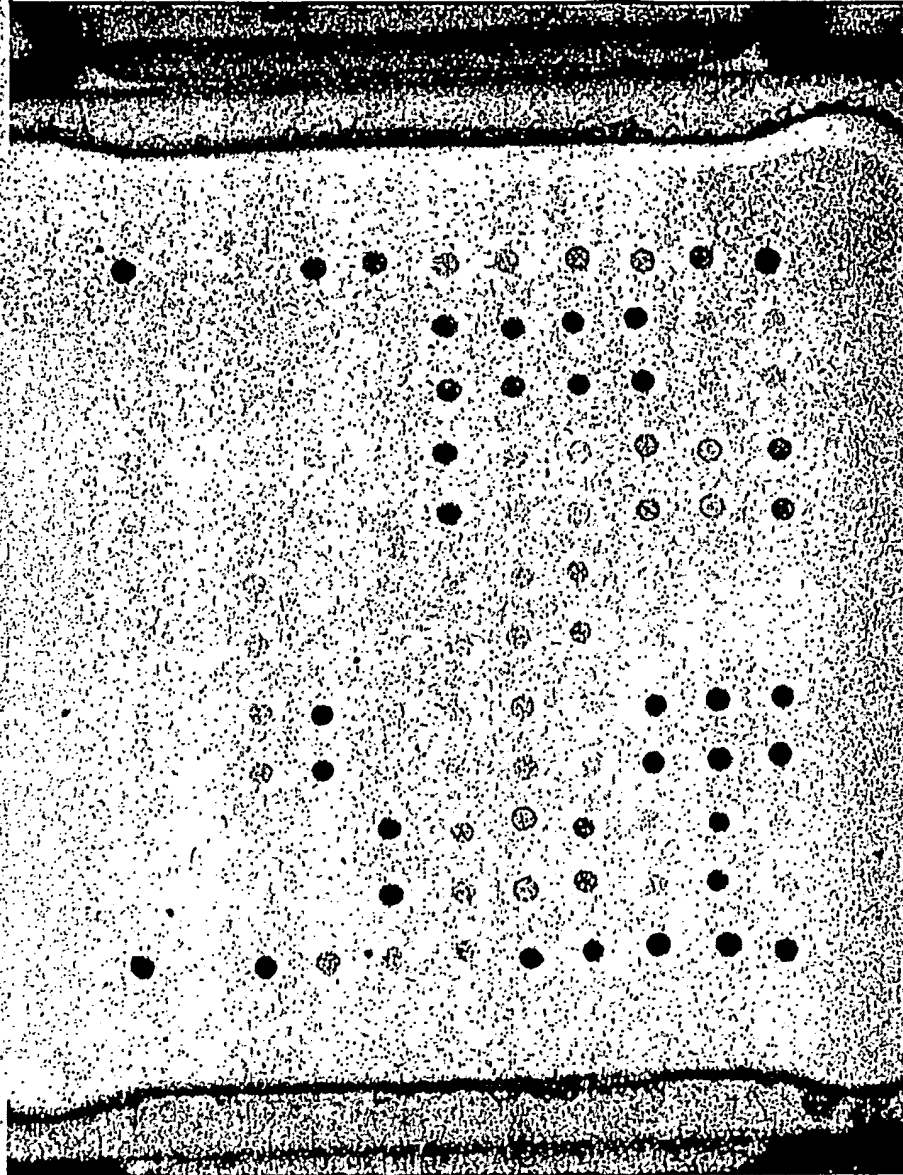
P. aeruginosa AT-Chip



KB1-85

Fig.13

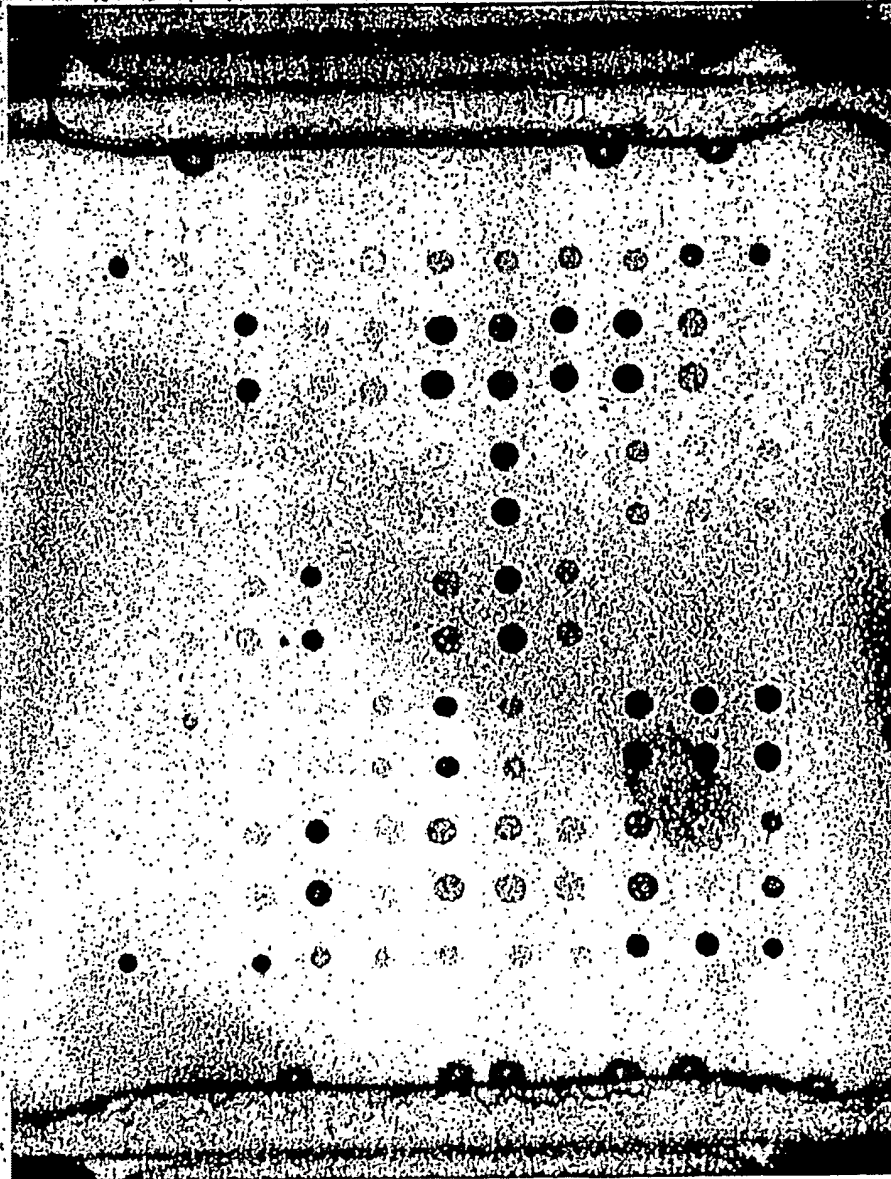
P. aeruginosa AT-Chip



ZW98

Fig.14

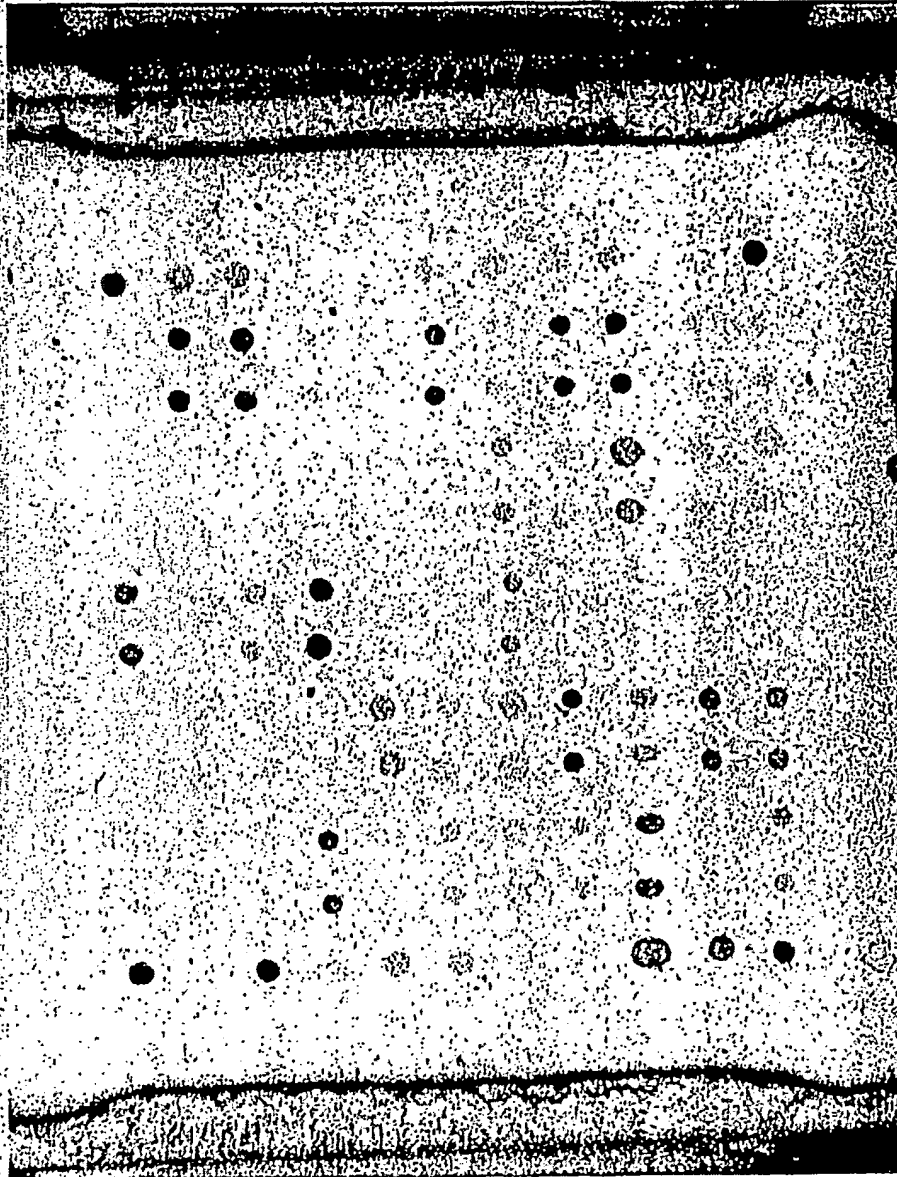
P. aeruginosa AT-Chip



641HD

Fig.15

P. aeruginosa AT-Chip



ATCC15522

Fig.16

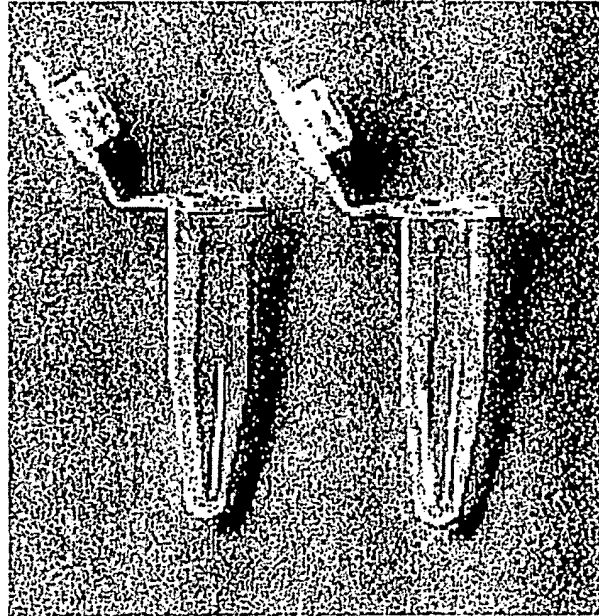


Fig.17a

47-1/23
ACGCGGATGTCCTGGATTGG

47-1/39
CTGAAGAAGGGGCGCTACGCG

47-2/22
GCGTACCGGGCAAGGTGATAG

47-2/52
CTCGGTGAAACATCGGGAGGG

C45/18
TCATCCAGCAAGCCATTGCGC

C45/60a
GGAGTCGCTTTCGCCCATCG

C45/60b
TGGAGTCGCTTTCGCCCATCG

C46/15
AAGGGCGTTTCACGCTGACGC

C46/22
ATCCGGAAGGGCGTTTCACG

C46/88
TCCACACCTCAGACTTCGGCG

C47-1/43
TATTGACGACCTACCGCGCGC

C47-2/56a
GCAACTGATGTTCGCCCAGC

C47-2/56b
CGCAACTGATGTTCGCCCAGC

C47-2/59
ACACGCAACTGATGTTGCCCC

CIS-4/36
TGTCCCGGCTCAGTTCAACG

CIS-4/50
AACACCTTGGCGTTTGTCCC

CIS-4/51
GCAACACCTTGGCGTTTGTCC

CIS-5/4
TCAAGCTCGTTGTGGACCGC

CIS-5/48
GTTACGACGGCGTGCTGTCGG

CSP-1/39a
ACGCAACGTATTTCGGCGACCC

CSP-1/39b
CGCAACGTATTTCGGCGACCC

Fig.17b

fliAT/28
AGCTGATGGTATCGCCGTCGC

fliAT/72
CTAGTGATCGCACCGGAGCC

oriC/20
AGCCTCGACACCGGTTCTCG

oriC/54
TCGTTTCATCCCCAGGCTTCG

oriC/59
ACCATCTCGTTCATCCCCAGG

oprL/53
TTCTGAGCCCAGGACTGCTCG

oprL/65
TCGACGCGACGGTTCTGAGCC

fliCb/36
TGACGTTCTCGCCGGTAGCG

fliCb/65
CAGTAGCGGTACCGGTCTGCG

fliCb/66
CAGTAGCGGTACCGGTCTGC

alkAG/27
TTCCTCGCCGGCATAGTAGGC

alkGA/32

alkGA/51
CGAGGACGAGGCATCTTCCGG

citAG/4
GCAGGTAGCAGGTTCCAGG

citAG/46
AACTGTTCCCTTCTGCGCGGCG

citGC/8
TGATCGGCTTGGTCTCGCAGG

citGC/11
GCTGATCGGCTTGGTCTCGC

citGC/75
GAGGCGTTCTGCTCGTGGTCG

oprI/12
TTTTTCCAGCATGCGCAGGG

oprI/17
GCTGGCTTTTTCCAGCATGCG

oprI/22
TTGCGGCTGGCTTTTTCCAGC

am7CA/1
TTGGGATAGTTGCGGTTGGC

am7CA/27
CGTAGGCGATCTTCACCCGC

am7CA/29
TGGCGTAGGCGATCTTCACCC

am3CT/21
GGCGAGATAGCCGAACAGGC

am3CT/22
GCGGCGAGATAGCCGAACAGG

am3CT/69
CACTTGCTGCTCCATGAGCC

am2CT/35
GAGGTCGAGCAGGCTGATGC

am2CT/42
TAGGTCGCGAGGTCGAGCAGG

am2CT/92
GTCCTTCTGCACCGAGTCGG

am1GA/49
CGCATCTTGTCTGGGTCAGG

am1GA/58
TCGTCGAGGCGCATCTTGTCC

am45/1
ACGTCGAGGTGGGTCTGTTCCG

am45/96
GTAGCCTTCGGCATCCAGCG

am6TC/60
TCGGCATTGGGATAGTTGCGG

GI11/15
CCTCCTGTCTCATGCCGATGC

GI11/59
GCATTGCCACGGAAGGAAGG

GI11/71
GAAGGCATCATGGCATTGCGC

GI18/62
GTCATGGGGTTTCCCAGAGACC

fliCa/41
GATCGCGATGTCGACGGTGCC

fliCa/42
CGATCGCGATGTCGACGGTGCC

fliCa/46
TGCCGATCGCGATGTCGACG

Fig.17d

SG-1/40
GACGAATACCCAGCTGCGTGG

SG-1/43
GCAGACGAATACCCAGCTGCG

SG-4/1
CGCGACGTCGTGACGTCAGC

SG-4/67
ACTTTCGGCTCTTCGGGCTGG

TB46/21
AGGTAGAGACTCGGGGGAACC

TB46/45
TCGTTTTTCGGTCATGGCCAGG

TB471/22
TTCGCGACGAACATCCGTGG

TB471/25
CGCTTCGCGACGAACATCCG

TB472/36
GGATCGCTTCGATAGGGCAGC

TB472/84
AGAGGCATGGGTCTGTACCG

TB473/34
TCTGTCAATCCCCTTTGGGG

TB473/41
AGCCCCTTCTGTCAATCCCC

TB474/36
GGCTTCCTACCGAAGGTCAGG

TB474/41
TGAGGGCTTCCTACCGAAGG

exoS/31
TTCAAGGTCATGGGCAATGCC

exoS/37
AGTCCCTTCAAGGTCATGGGC

exoU/22
GCCGACTGAGCTGTAGCTCGG

exoU/23
GGCCGACTGAGCTGTAGCTCG

exoU/42
ACCAGACTGGTCAATGGTGG

flins/2
CCCGTGTTCCGTAGACCTTGC

pKL11/49a
AGCAGTTACCCACAGCATGG

Fig.17e

pKL11/49b
CAGCAGTTACCCACAGCATGG

pKL3/47
CTACACTCCAACCGCTGGTCC

pKL3/50
GACCTACACTCCAACCGCTGG

pKL3/80
TTCCCTTGCTGCCGAGAAGC

pKL7/14
TAATAGGCGAGCCTGCCGTCC

47D7nw1a
TCCACGCCGAGGGACGTGCC

47D7nw1b
GCTCCACGCCGAGGGACGTGCC

C46-nw1a
CGCGGTGCTGGTTGCGCTGC

C46-nw1b
CCAATGCCCAGGGCCAGCGGA

C46-nw1c
CGCTGGCAGTTCCGCTGGCC

ExoSnw1a
CAGGGTCGCCAGCTCGCTCGCC

ExoSnw1b
AGGGTCGCCAGCTCGCTCGC

ExoUnw1a
AGTGATCTGCCGCGGCCCTGCC

ExoUnw1b
GTGATCTGCCGCGGCCCTGC

OrfA-1
GTTCCACAGGCGCTGCGGCGC

OrfA-2
GTTCCACAGGCGCTGCGGCG

OrfA-3
CAAAGCCCCTGGTCGCGCGG

OrfC-1
GCAGCTTTTCCACGCGCGGCGG

OrfI-1
AAACTGCCCCGCCCCCATCC

OrfI-2
GGAAAACTGCCCCGCCCCC

OrfJ-1
ACGCTCGCAGCGCCTCACGCG

OrfJ-2
GGCCTGGCTGCGAACGCTCGC

Fig.17f

Fig.18a

no	tube	name	5'-3'-sequence	group	length	GC-content [%]	Tm [°C]	spot-ID's
1	Pa-S_001	oriC T-C_wt	GAAGCCGAGCAATGCGTGTTC	1	23	52,2	62,4	2,3
2	Pa-S_056	oriC T-C_mut_1	GAAGCCGAGCAACTGCGTGTTC	1	23	56,5	64,2	14,15
3	Pa-S_057	oprL T-C_wt_1	GGTGCTGCAGGTTTCGCCGG	1	23	69,6	69,6	4,5
4	Pa-S_058	oprL T-C_mut_1	GGTGCTGCAGGCGTTTCGCCGG	1	23	73,9	71,3	16,17
5	Pa-S_059	fliC a A-T_wt_1	CAAGATCGCCGACGGTCAAC	1	22	63,6	65,8	6,7
6	Pa-S_060	fliC a A-T_mut_1	CAAGATCGCCGCTCGGTCAAC	1	22	63,6	65,8	18,19
7	Pa-S_061	alkB2 G-A_wt_1	TGCTGCTGGCGGCGGTGTGCTAT	1	23	65,2	67,8	8,9
8	Pa-S_062	alkB2 G-A_mut_1	TGCTGCTGGCAGCGGTGTGCTAT	1	23	60,9	66,0	20,21
9	Pa-S_063	alkB2 A-G_wt_1	CCTCGCCCTGTTCACACCGCTCTGG	1	25	72,0	72,8	10,11
10	Pa-S_064	alkB2 A-G_mut_1	CTCGCCCTGTTCACACCGCTCTGG	1	24	75,0	73,0	22,23
11	Pa-S_065	citS A-G_wt_1	TCGAGCAACTGGCAGAGAAATCCG	1	24	54,2	64,4	26,27
12	Pa-S_066	citS A-G_mut_1	CGAGCAACTGGCGGAGAAATCCG	1	23	60,9	66,0	38,39
13	Pa-S_067	citS G-C_wt_1	GCGGAAACTTCCTGCACATGATGTT	1	26	46,2	63,2	28,29
14	Pa-S_068	citS G-C_mut_1	GCGGAAACTTCCTCCACATGATGTT	1	26	46,2	63,2	40,41
15	Pa-S_069	oprI T-C_wt_1	AGCTCAGCAGACTGCTGACGAGG	1	23	60,9	66,0	30,31
16	Pa-S_070	oprI T-C_mut_1	AGCTCAGCAGACCGCTGACGAG	1	22	63,6	65,8	42,43
17	Pa-S_071	ampC_1 G-A_wt_1	AAGAGGACGGCCCGGGTGACGCC	1	25	76,0	74,5	32,33
		ampC_1 G-						
18	Pa-S_072	A_mut_1	AAGAGGACGGCCCGCAGGTGACCGG	1	26	73,1	74,3	44,45
19	Pa-S_019	ampC_2 C-T_wt	GACAAGATGGCCTCGACGACC	1	22	63,6	65,8	34,35
		ampC_2 C-						
20	Pa-S_073	T_mut_1	GACAAGATGCGTCTCGACGACCG	1	23	60,9	66,0	46,47
21	Pa-S_021	ampC_3 C-T_wt	AGCCGACCTACGCGCGGGCAG	1	22	77,3	71,4	50,51
		ampC_3 C-						
22	Pa-S_074	T_mut_1	CAGCCGACCTATGCGCCGGGCAG	1	23	73,9	71,3	62,63
23	Pa-S_075	ampC_4 G-A_wt_1	CCGTTTGAACGGCTCATGGAGCA	1	23	60,9	66,0	52,53
		ampC_4 G-						
24	Pa-S_076	A_mut_1	GCCGTTTGAACGACTCATGGAGCA	1	24	58,3	66,1	64,65
25	Pa-S_077	ampC_5 G-C_wt_1	TGGAGCAGCAAGTGTTCGCCGGC	1	22	63,6	65,8	54,55

Fig.18b

25	Pa-S_078	ampC_5 G-	TGGAGCAGCAACTGTTCCCGGC	1	22	63,6	65,8	66,67
27	Pa-S_027	ampC_6 T-C_wt	GAACAAGACCGGTTCCACCAACGG	1	24	58,3	66,1	56,57
28	Pa-S_079	ampC_6 T-	AACAAGACCGGCTCCACCAACGG	1	23	60,9	66,0	68,69
29	Pa-S_029	ampC_7 C-A_wt	GCGACCTGGGCCTGGTGATCCT	1	22	68,2	67,7	58,59
30	Pa-S_080	ampC_7 C-	GCGACCTGGGACTGGTGATCCT	1	22	63,6	65,8	70,71
31	Pa-S_031	A_mut_1	GCCGACCACTGAATCCAACTCG	2	24	58,3	66,1	74,75
32	Pa-S_032	flhC b	GTCGCTGAACGGCACCTACTTCA	2	23	56,5	64,2	86,87
33	Pa-S_033	exoS-1	CAGCCTGGGTCATGTCTCTCGG	3	22	68,2	67,7	76,77
34	Pa-S_034	exoU	CGCCAGTTTGAGAACGGAGTCACC	3	24	58,3	66,1	88,89
35	Pa-S_038	C-47-1	GCGCGATCTTCTCCACTTCATCGG	4	24	54,2	64,4	78,79
36	Pa-S_039	C-47-2	GCCTCCGCGATTGAACATCGTGAT	4	24	58,3	66,1	90,91
37	Pa-S_040	47D7-1	GTAGCCGGAGTCGAGCGGAATCAT	5	24	54,2	64,4	80,81
38	Pa-S_041	47D7-2	GTAGCATGGAATCGGCAGTCGTT	5	24	58,3	66,1	92,93
39	Pa-S_054	C-45	CGAGGAGTTTGGACCGGCTTTCG	6	24	54,2	64,4	82,83
40	Pa-S_055	C-46	AATAGGACCGGCAGAACGGGCATT	6	24	58,3	66,1	94,95
41	Pa-S_035	C-inselspez-4	GCGCCTCTCTCTCTTTCGAGATGT	7	24	54,2	64,4	86,88
42	Pa-S_036	C-inselspez-5	CAGTATGGTACGGACACGAAGCGC	7	24	58,3	66,1	110,111
43	Pa-S_037	C-spezifisch-1	GCATCATTCGCGGTGAGATCTGCT	8	24	58,3	66,1	122,123
44	Pa-S_044	pKL-3	TCTGAACCTGGCGCTATCACCTGGA	9	24	54,2	64,4	100,101
45	Pa-S_045	pKL-7	AATTGATGGCTTCTCAGGCGCAGG	9	24	54,2	64,4	112,113
46	Pa-S_046	pKL-11	AGTCATGGGACTGAATACGGCGACT	9	25	52,0	64,6	124,125
47	Pa-S_042	PAGI-1-1	TTCCTCGGTGTCGAGGGATTCCTGG	10	24	58,3	66,1	102,103
48	Pa-S_043	PAGI-1-8	TGGTAGCTCTCGACGTACTGGCTG	10	24	58,3	66,1	114,115
49	Pa-S_047	SG17M-1	CCCGTTGCTCATAAACCGGTTCTCTG	11	24	58,3	66,1	104,105
50	Pa-S_048	SG17M-4	AGGGCATTCCTCAGGTGGACTCAGG	11	24	54,2	64,4	116,117
51	Pa-S_053	fla-insel-1	AGCTGTGTCGGTGGAGGCTATGTT	12	24	58,3	66,1	106,107
52	Pa-S_049	TB-C47-1	AGCTGCCCTGACCAAGCTCATACG	13	24	58,3	66,1	118,119
53	Pa-S_050	TB-C47-2	CGCCAAACAATTCGCCATTACAGCG	13	24	54,2	64,4	126,127
54	Pa-S_051	TB-C47-3	TCCAAACAGGCAGGAGTACAGGGTG	13	24	58,3	66,1	128,129

55	Pa-S_052	TB-C47-4	CGCTGCACATACAGGTCGGTTCTC	13	24	54,2	64,4	130,131
56	Biotin + Cy3-marker							1,12,97,121,132
57	Pa-S_081	oriC T-C_wt_1	AGCCACGCAATTGCGTGTTCCTCCG	1	25	65,6	56	
58	Pa-S_082	oriC T-C_mut_2	AGCCACGCAACTGCGTGTTCCTCC	1	24	65,1	58	
59	Pa-S_083	alkB2 G-A_wt_2	GCTGCTGGCGGGTGTGC		19	67,4	79	8,9
60	Pa-S_084	alkB2 G-A_mut_2	TGCTGCTGGCAGCGGTGTGCT		21	67,3	67	20,21
61	Pa-S_085	oprI T-C_wt_2	CAGAAAGCTCAGCAGACTGCTGACGAG		27	64,6	56	
62	Pa-S_086	oprI T-C_mut_2	GAAAGCTCAGCAGACCGCTGACGAG		25	64,9	60	
63	Pa-S_087	ampC_1 G-A_wt_2	ACGGCCGCCGGGTGACGCC		19	70,2	84	
		ampC_1 G-						
64	Pa-S_088	A_mut_2	ACGGCCGCCAGGTGACGCCG		20	69,9	80	
65	Pa-S_089	ampC_3 C-T_wt_1	GCCGACCTACGCCGCCGGGC		19	68,4	84	
		ampC_3 C-						
66	Pa-S_090	T_mut_2	AGCCGACCTATGCGCCGGGCA		21	68,4	71	
67	Pa-S_091	ampC_4 G-A_wt_2	GTTCGAACGGCTCATGGAGCAGCA		24	65	58	
		ampC_4 G-						
68	Pa-S_092	A_mut_2	GTTCGAACGACTCATGGAGCAGCAAG		26	63,5	54	
69	Pa-S_093	exoS-1_1	CAGCCACAGTCAGGACGCGCA		20	64,9	70	
70	Pa-S_094	exoU_1	AGTGACGTGCGTTTCAGCAGTCCC		24	64,8	58	
71	Pa-S_095	47D7-1_1	GTGTCACGGCCCATGTCTAGCAGC		24	65	63	
72	Pa-S_096	C-46_1	CGAAGTCTGAGGTGTGGACCCGC		23	64,5	65	
73	Pa-S_097	Fla-Insel-2_orfA	CGCTGGAGGGTATGTTCCGCAAGG		24	64,8	63	
74	Pa-S_098	Fla-Insel-2_orfC	CGTACTCAGCTTCTCCACCCAGCG		24	64,3	63	
75	Pa-S_099	Fla-Insel-2_orfI	CCTGGACCTCTCCAAGGTTCCGCT		24	65	63	
76	Pa-S_100	Fla-Insel-2_orfJ	GCCATTCCGACGACCAACCAAGGC		24	64,2	58	

group "mother"

Fig.18c

well- no	tube	name	5'-3'-sequence	group	length	GC- content [%]	Tm [°C]	spot- ID's
1	Pa-S_001	oriC T-C_wt	GAAGCCCAAGCAATTGCGGTTC	1	23	52,2	62,4	23
2	Pa-S_056	oriC T-C_mut_1	GAAGCCCAAGCAACTGCGGTTC	1	23	56,5	64,2	14,15
57	Pa-S_081	oriC T-C_wt_1	AGCCCAAGCAATTGCGGTTC	1	25	65,6	56	13,25
58	Pa-S_082	oriC T-C_mut_2	AGCCCAAGCAACTGCGGTTC	1	24	65,1	58	37,49
3	Pa-S_057	oprL T-C_wt_1	GGTGTGTCAGGGTGTTCGCCGG	1	23	69,6	69,6	4,5
4	Pa-S_058	oprL T-C_mut_1	GGTGTGTCAGGGCGTTTCGCCGG	1	23	73,9	71,3	16,17
5	Pa-S_059	fliC a A-T_wt_1	CAAGATCGCCCGCAGCGGTCAAC	1	22	63,6	65,8	6,7
6	Pa-S_060	fliC a A-T_mut_1	CAAGATCGCCCGCTGCGGTCAAC	1	22	63,6	65,8	18,19
59	Pa-S_083	alkB2 G-A_wt_2	GCTGTGGCGGGCGGTGTC	1	19	67,4	79	8,9
60	Pa-S_084	alkB2 G-A_mut_2	TGCTGTGGCAGCGGTGTC	1	21	67,3	67	20,21
9	Pa-S_063	alkB2 A-G_wt_1	CCTCGCCCTGTTCACCGCTCTGG	1	25	72,0	72,8	10,11
10	Pa-S_084	alkB2 A-G_mut_1	CTCGCCCTGTTCACCGCTCTGG	1	24	75,0	73,0	22,23
11	Pa-S_065	citS A-G_wt_1	TCGAGCAACTGGCAGAGAAATCCG	1	24	54,2	64,4	26,27
12	Pa-S_066	citS A-G_mut_1	CGAGCAACTGGCGGAGAAATCCG	1	23	60,9	66,0	38,39
13	Pa-S_067	citS G-C_wt_1	GCGGAAACTTCCTGCACATGATGTT	1	26	46,2	63,2	28,29
14	Pa-S_068	citS G-C_mut_1	GCGGAAACTTCCTCCACATGATGTT	1	26	46,2	63,2	40,41
15	Pa-S_039	oprI T-C_wt_1	AGCTCAGCAGACTGCTGACGAGG	1	23	60,9	66,0	30,31
16	Pa-S_070	oprI T-C_mut_1	AGCTCAGCAGACCGCTGACGAG	1	22	63,6	65,8	42,43
61	Pa-S_085	oprI T-C_wt_2	CAGAAAGCTCAGCAGACTGCTGACGAG	1	27	64,6	56	61,73
62	Pa-S_086	oprI T-C_mut_2	GAAAGCTCAGCAGACCGCTGACGAG	1	25	64,9	60	24,85
63	Pa-S_087	ampC_1 G-A_wt_2	ACGGCCCGCGGGTGACGCC	1	19	70,2	84	32,33
64	Pa-S_088	ampC_1 G-A_mut_2	ACGGCCCGCAGGTGACGCCG	1	20	69,9	80	44,45
19	Pa-S_019	ampC_2 C-T_wt	GACAAGATGCGCCCTCGACGACC	1	22	63,6	65,8	34,35
20	Pa-S_073	ampC_2 C-T_mut_1	GACAAGATGCGTCTCGACGACCG	1	23	60,9	66,0	46,47
21	Pa-S_021	ampC_3 C-T_wt	AGCCGACCTACGCGCCGGGCAG	1	22	77,3	71,4	50,51
22	Pa-S_074	ampC_3 C-T_mut_1	CAGCCGACCTATGCGCCGGGCAG	1	23	73,9	71,3	62,63

Fig.19a

Fig.19b

65	Pa-S_069	ampC_3 C-T_wt_1	GCCGACCTACGGCGCCGGGC	1	19	68,4	84	36,48
66	Pa-S_090	ampC_3 C-T_mut_2	AGCCGACCTATGCGCGGGCA	1	21	68,4	71	60,72
67	Pa-S_091	ampC_4 G-A_wt_2	GTTCGACCGGCTCATGGAGCAGCA	1	24	65	58	52,53
68	Pa-S_092	ampC_4 G-A_mut_2	GTTCGAACGACTCATGGAGCAGCAAG	1	26	63,5	54	64,65
25	Pa-S_077	ampC_5 G-C_wt_1	TGGAGCAGCAAGTGTTCCCGGC	1	22	63,6	65,8	54,55
26	Pa-S_078	ampC_5 G-C_mut_1	TGGAGCAGCAACTGTTCCTCCGGC	1	22	63,6	65,8	66,67
27	Pa-S_027	ampC_6 T-C_wt	GAACAAGACCGGTTCCACCAACGG	1	24	58,3	66,1	56,57
28	Pa-S_079	ampC_6 T-C_mut_1	AACAAGACCGGCTCCACCAACGG	1	23	60,9	66,0	68,69
29	Pa-S_029	ampC_7 C-A_wt	GCGACCTGGGCTGGTGATCCT	1	22	68,2	67,7	58,59
30	Pa-S_080	ampC_7 C-A_mut_1	GCGACCTGGGACTGGTGATCCT	1	22	63,6	65,8	70,71
31	Pa-S_031	flc b	GCCGACCAACTGACTCCACTCG	2	24	58,3	66,1	74,75
32	Pa-S_032	flc a	GTGCTGAACGGCACCTACTCA	2	23	56,5	64,2	86,87
69	Pa-S_093	exoS_1_1	GAGCCAGTCAAGACGGCA	3	20	64,9	70	76,77
34	Pa-S_034	exoU	CGCCAGTTTGAGAACGGAGTCACC	3	24	58,3	66,1	88,89
70	Pa-S_094	exoU_1	AGTGACGTGCGTTTCAGCAGTCCC	3	24	64,8	58	84,96
35	Pa-S_038	C-47-1	GCGGATCTTCTGCACTTCAATCGG	4	24	54,2	64,4	78,79
71	Pa-S_095	47D7-1_1	GTGTCACGGCCCATGCTAGCAGC	5	24	65	63	80,81
38	Pa-S_041	47D7-2	GTGAGCATGGAATCGGCAGTCGTT	5	24	58,3	66,1	92,93
39	Pa-S_054	C-45	CGAGGACTTTCGGACCGGCTTGA	6	24	54,2	64,4	82,83
40	Pa-S_055	C-46	AATAGGACCGGCAGAACGGGCATT	6	24	58,3	66,1	94,95
72	Pa-S_096	C-46_1	CGAAGTCTGAGGTGTGGACCCGC	6	23	64,5	65	108,120
41	Pa-S_035	C-Insel spez. 4	GCGCCTTCTCCTCTTTGCAGATGT	7	24	54,2	64,4	98,99
42	Pa-S_036	C-Insel spez. 5	CAGTATGGTACGGACACGAAGCGC	7	24	58,3	66,1	110,111
43	Pa-S_037	C-spezifisch-1	GCATCATTCGCGCTCAGATCTGGT	8	24	58,3	66,1	122,123
44	Pa-S_044	pKL-3	TCTGAATGCGGCTATCAGCTGGA	9	24	54,2	64,4	100,101
46	Pa-S_046	pKL-11	AGTCATGGGACTGAATACGGCGACT	9	25	52,0	64,6	124,125
47	Pa-S_042	PAGI-1-1	TTCTCGGTGTCGAGGATTTCTCGG	10	24	58,3	66,1	102,103
48	Pa-S_043	PAGI-1-8	TGGTAGCTCTCGACGTAAGTGGCTG	10	24	58,3	66,1	114,115

49	Pa-S_047	SG17M-1	CCCGTTGCTCATAACCCGTTCTG	11	24	58,3,66,1,104,105
50	Pa-S_048	SG17M-4	AGGGCATTCTCAGGTGGACTCAGG	11	24	54,2 64,4 116,117
51	Pa-S_053	fla-insel-1	ACCTGTGTCGCTGGGCGGTATGTT	12	24	58,3 66,1 106,107
54	Pa-S_051	TB-C47-3	TCCACAGGCGAGGAGTACAGGGTG	13	24	58,3 66,1 128,129
55	Pa-S_052	TB-C47-4	CGCTGCACATACAGGTCGGTTCTC	13	24	54,2 64,4 130,131
73	Pa-S_057	Fla-Insel-2_orfA	CGCTGGAGGGTATGTTCCGCAAGG	14	24	64,8 63 90,91
74	Pa-S_098	Fla-Insel-2_orfC	CGTACTCAGCTTCTCCACCCACGG	14	24	64,3 63 112,113
75	Pa-S_099	Fla-Insel-2_orfI	CCTGGACCTCTCCAAAGGTTCCGCT	14	24	65 63 118,119
76	Pa-S_100	Fla-Insel-2_orfJ	GCCATTCGACGACCAACAAGGC	14	24	64,2 58 126,127
56	Biotin + Cy3-marker					1,12,97,121,132
	group "mother"					

Fig.19c

Fig.20

Chip: MHH_P_aer_array2 (12x11 array with spot distance of 19.00 mm)

56	43	43	46	46	76	76	54	54	55	55	56
	42	42	74	74	48	48	50	50	75	75	72
56	41	41	44	44	47	47	49	49	51	51	72
62	32	32	34	34	73	73	38	38	40	40	70
61	31	31	69	69	35	35	71	71	39	39	70
61	22	22	68	68	26	26	28	28	30	30	66
58	21	21	67	67	25	25	27	27	29	29	66
58	12	12	14	14	16	16	64	64	20	20	65
57	11	11	13	13	15	15	63	63	19	19	65
57	2	2	4	4	6	6	60	60	10	10	62
56	1	1	3	3	5	5	59	59	9	9	56

Fig.21

Chip occupancy

marker spot	C-spezifisch-1	pKL-11	Fla-Insel-2_orfJ	TB-C47-3	TB-C47-4	marker spot
marker spot	C-Insel-spezifisch-5	Fla-Insel-2_orfC	PAGI-1-8	SG17M-4	Fla-Insel-2_orfI	C-46_1
	C-Insel-spezifisch-4	pKL-3	PAGI-1-1	SG17M-1	fla-Insel-1	C-46_1
mut_2 oprl T-C wt_2	flic A	exoU	Fla-Insel-2_orfA	47D7-2	C-46	exoU_1
	flic B	exoS-1_1	C-47-1	47D7-1_1	C-45	exoU_1
mut_2 oriC T-C wt_1	mut_1 ampC_3 C-T wt	mut_2 ampC_4 G-A wt_2	mut_1 ampC_5 G-C wt_1	mut_1 ampC_6 T-C wt	mut_1 ampC_7 C-A wt	mut_2 ampC_3 C-T mut_2 ampC_3 C-T wt_1 ampC_3 C-T wt_1
	mut_1 citS A-G wt_1	mut_1 citS G-C wt_1	mut_1 oprl T-C wt_1	mut_2 ampC_1 G-A wt_2	mut_1 ampC_2 C-T wt	
marker spot	mut_1 oriC T-C wt	mut_1 oprl T-C wt_1	mut_1 flic a A-T wt_1	mut_2 alkB2 G-A wt_2	mut_1 alkB2 A-G wt_1	oprl T-C mut_2 marker spot